

CLAIMS:

1. A B Lymphocyte Stimulator (BLyS) binding polypeptide comprising the amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.
2. The polypeptide according to Claim 1, wherein Xaa is Pro or Ser.
3. The polypeptide according to Claim 1, wherein said polypeptides comprises the amino acid sequence: $X_1-X_2-\text{Asp}-X_4-\text{Leu}-\text{Thr}-X_7-\text{Leu}-X_9-X_{10}$ (SEQ ID NO:448), wherein

X_1 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X_2 is Tyr, Phe, Glu, Cys, Asn;

X_4 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X_7 is Lys, Asn, Gln, Gly, or Arg;

X_9 is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and

X_{10} is Leu, Phe, Val, Ile, or His.

4. The polypeptide according to Claim 3, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

5. The polypeptide according to Claim 3, wherein said polypeptide comprises the amino acid sequence: Ala- $X_2-X_3-X_4-\text{Asp}-X_6-\text{Leu}-\text{Thr}-X_9-\text{Leu}-X_{11}-X_{12}-X_{13}-X_{14}$ (SEQ ID NO:447),

wherein

X_2 is any amino acid except Arg;

X_3 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X_4 is Tyr, Phe, Glu, Cys, Asn;

X_6 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X_9 is Lys, Asn, Gln, Gly, or Arg;

X_{11} is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X₁₂ is Leu, Phe, Val, Ile, or His;

X₁₃ is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X₁₄ is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

6. The polypeptide according to Claim 3, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 186-435 as depicted in Table 14.

7. The polypeptide according to Claim 3, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 437-444 as depicted in Table 15.

8. The polypeptide according to Claim 1, comprising an amino acid sequence selected from the group consisting of:

Ala-Gly-Lys-Glu-Pro-Cys-Tyr-Phe-Tyr-Trp-Glu-Cys-Ala-Val-Ser-Gly (SEQ ID NO:450);

Ala-Gly-Val-Pro-Phe-Cys-Asp-Leu-Leu-Thr-Lys-His-Cys-Phe-Glu-Ala-Gly (SEQ ID NO:451);

Gly-Ser-Ser-Arg-Leu-Cys-His-Met-Asp-Glu-Leu-Thr-His-Val-Cys-Val-His-Phe-Ala-Pro (SEQ ID NO:452);

Gly-Asp-Gly-Gly-Asn-Cys-Tyr-Thr-Asp-Ser-Leu-Thr-Lys-Leu-His-Phe-Cys-Met-Gly-Asp-Glu (SEQ ID NO:453);

Gly-Tyr-Asp-Val-Leu-Thr-Lys-Leu-Tyr-Phe-Val-Pro-Gly-Gly (SEQ ID NO:454);

Trp-Thr-Asp-Ser-Leu-Thr-Gly-Leu-Trp-Phe-Pro-Asp-Gly-Gly (SEQ ID NO:455);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:186);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:456);

Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:457);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Val (SEQ ID NO:189);

Ala-Asn-Trp-Phe-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:309);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Ser-Leu-Pro-Asp (SEQ ID NO:458);

Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Phe-Pro-Asp (SEQ ID NO:353);

Ala-Asn-Trp-Tyr-Asp-Ser-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:327).

9. A BLyS binding polypeptide comprising an amino acid sequence according to one of the following formulae:

(H) Cys-X₂-Phe-X₄-Trp-Glu-Cys (SEQ ID NO:8),

wherein

X₂ is Phe, Trp, or Tyr; and

X₄ is Pro or Tyr; or

(I) Cys-X₂-X₃-X₄-X₅-X₆-X₇-Cys (SEQ ID NO:9),

wherein

X₂ is Asp, Ile, Leu, or Tyr;

X₃ is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X₄ is His, Leu, Lys, or Phe;

X₅ is Leu, Pro, or Thr;

X₆ is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp; and

X₇ is Ala, Asn, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val; or

(J) Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (SEQ ID NO:10),

wherein

X₂ is Asn, Asp, Pro, Ser, or Thr;

X₃ is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X₄ is Ala, Ile, Leu, Pro, Thr, or Val;

X₅ is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X₆ is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X₇ is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X₈ is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr; or

(K) Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-Cys (SEQ ID NO:11),

wherein

X₂ is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X₃ is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X₄ is Asp, His, Leu, or Ser;

X₅ is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X₆ is Ala, Arg, Asn, or Leu;

X₇ is Ile, Leu, Met, Pro, Ser, or Thr;

X₈ is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X₉ is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val; or

(L) Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys (SEQ ID NO:12),

wherein

X₂ is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X₃ is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X₄ is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X₅ is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;

X₆ is Asp, Leu, Pro, Thr, or Val;

X₇ is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;

X₈ is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;

X₉ is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;

X₁₀ is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr; and

X₁₁ is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val.

10. The polypeptide according to Claim 9, wherein

(a) said polypeptide comprises an amino acid sequence of the formula:

Cys-X₂-Phe-X₄-Trp-Glu-Cys (SEQ ID NO:8), and the following amino acid positions are independently selected as follows: X₂ is Tyr; X₄ is Pro; or combinations of such selections; or

(b) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X₂-X₃-X₄-X₅-X₆-X₇-Cys (SEQ ID NO:9), and the following amino acid positions are independently selected as follows: X₂ is Asp or Leu; X₃ is Glu or Leu; X₄ is His or Leu; X₅ is Thr or Pro; X₆ is Lys; or combinations of such selections; or

(c) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-Cys (SEQ ID NO:10),

and the following amino acid positions are independently selected as follows: X₂ is Asp; X₃ is Ile; X₄ is Val or Leu; X₅ is Thr; X₆ is Leu; X₈ is Ser; or combinations of such selections; or

(d) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-Cys (SEQ ID NO:11), and the following amino acid positions are independently selected as follows: X₄ is Asp; X₅ is Glu or Pro; X₆ is Leu; X₇ is Thr; or combinations of such selections; or

(e) said polypeptide comprises an amino acid sequence of the following formula:

Cys-X₂-X₃-X₄-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-Cys (SEQ ID NO:12),

and the following amino acid positions are independently selected as follows: X₂ is Trp, Tyr, or Val; X₃ is Asp; X₄ is Asp; X₅ is Leu; X₆ is Leu or Thr; X₇ is Lys or Thr; X₈ is Arg or Leu; X₉ is Thr or Trp; X₁₀ is Met or Phe; X₁₁ is Val; or combinations of such selections.

11. A BLyS binding polypeptide comprising an amino acid sequence of the following formula:

(A) X₁-X₂-X₃-Cys-X₅-Phe-X₇-Trp-Glu-Cys-X₁₁-X₁₂-X₁₃ (SEQ ID NO:1),

wherein

X₁ is Ala, Asn, Lys, or Ser;

X₂ is Ala, Glu, Met, Ser, or Val;

X₃ is Ala, Asn, Lys, or Pro;

X₅ is Phe, Trp, or Tyr;

X₇ is Pro or Tyr;

X₁₁ is Ala, Gln, His, Phe, or Val;

X₁₂ is Asn, Gln, Gly, His, Ser, or Val; and

X₁₃ is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-Cys-X₁₂-X₁₃-X₁₄ (SEQ ID

NO:2),

wherein

X₁ is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X₂ is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X₅ is Asp, Ile, Leu, or Tyr;

X₆ is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X₇ is His, Leu, Lys, or Phe;

X₈ is Leu, Pro, or Thr;

X₉ is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X₁₀ is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X₁₂ is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X₁₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X₁₄ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—Cys—X₁₃—X₁₄—X₁₅ (SEQ ID NO:3),

wherein

X₁ is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X₂ is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X₃ is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X₅ is Asn, Asp, Pro, Ser, or Thr;

X₆ is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X₇ is Ala, Ile, Leu, Pro, Thr, or Val;

X₈ is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X₉ is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X₁₀ is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X₁₁ is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X₁₃ is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X₁₄ is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X₁₅ is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—Cys—X₁₄—X₁₅—X₁₆

(SEQ ID NO:4),

wherein

X₁ is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X₂ is Arg, Asn, Asp, His, Phe, Ser, or Trp;
X₃ is Asn, Asp, Leu, Pro, Ser, or Val;
X₅ is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;
X₆ is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;
X₇ is Asp, His, Leu, or Ser;
X₈ is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;
X₉ is Ala, Arg, Asn, or Leu;
X₁₀ is Ile, Leu, Met, Pro, Ser, or Thr;
X₁₁ is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;
X₁₂ is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;
X₁₄ is Asp, Gly, Leu, Phe, Tyr, or Val;
X₁₅ is Asn, His, Leu, Pro, or Tyr; and
X₁₆ is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X₁-X₂-X₃-Cys-X₅-X₆-X₇-X₈-X₉-X₁₀-X₁₁-X₁₂-X₁₃-X₁₄-Cys-X₁₆-X₁₇-X₁₈

(SEQ ID NO:5),

wherein

X₁ is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;
X₂ is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;
X₃ is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;
X₅ is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;
X₆ is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;
X₇ is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;
X₈ is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;
X₉ is Asp, Leu, Pro, Thr, or Val;
X₁₀ is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;
X₁₁ is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;
X₁₂ is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;
X₁₃ is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;
X₁₄ is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;
X₁₆ is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;
X₁₇ is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr; and

X₁₈ is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F) X₁—X₂—X₃—X₄—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂ (SEQ ID NO:6),

wherein

X₁ is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;

X₂ is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;

X₃ is Ala, Asp, Lys, Phe, Thr, Trp or Tyr;

X₄ is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;

X₅ is Asp, Leu, Lys, Phe, Pro, Ser, or Val;

X₆ is His, Ile, Leu, Pro, Ser, or Thr;

X₇ is Arg, Gly, His, Leu, Lys, Met, or Thr;

X₈ is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;

X₉ is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;

X₁₀ is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;

X₁₁ is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and

X₁₂ is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G) X₁—X₂—X₃—X₄—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—X₁₃ (SEQ ID NO:7),

wherein

X₁ is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;

X₂ is Arg, Gln, His, Ile, Leu, or Pro;

X₃ is Asp, Gly, Ile, Lys, Thr, Tyr or Val;

X₄ is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;

X₅ is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;

X₆ is Asp, Glu, His, Leu, Lys, Pro, or Val;

X₇ is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;

X₈ is Gln, Gly, His, Leu, Met, Ser, or Thr;

X₉ is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;

X₁₀ is Ala, Gly, Ile, Leu, Lys, Met, or Phe;

X₁₁ is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;

X₁₂ is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and

X₁₃ is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

12. The BLyS binding polypeptide according to Claim 11, wherein

(a) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-\text{Cys}-X_5-\text{Phe}-X_7-\text{Trp}-\text{Glu}-\text{Cys}-X_{11}-X_{12}-X_{13}$ (SEQ ID NO:1), and the following amino acid positions are independently selected as follows: X_3 is Lys; X_5 is Tyr; X_7 is Pro; X_{11} is Ala, Gln, His, Phe, or Val; X_{12} is Asn, Gln, Gly, His, Ser, or Val; X_{13} is Ala, Asn, Gly, Ile, Pro, or Ser; or combinations of such selections; or

(b) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-\text{Cys}-X_5-X_6-X_7-X_8-X_9-X_{10}-\text{Cys}-X_{12}-X_{13}-X_{14}$ (SEQ ID NO:2), and the following amino acid positions are independently selected as follows: X_3 is Asp; X_5 is Asp or Leu; X_6 is Glu or Leu; X_7 is His or Leu; X_8 is Thr or Pro; X_9 is Lys; or combinations of such selections; or

(c) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-\text{Cys}-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-\text{Cys}-X_{13}-X_{14}-X_{15}$ (SEQ ID NO:3), and the following amino acid positions are independently selected as follows: X_3 is Ala; X_5 is Asp; X_6 is Ile; X_7 is Val or Leu; X_8 is Thr; X_9 is Leu; X_{11} is Ser; X_{13} is Val; X_{15} is Glu or Pro; or combinations of such selections; or

(d) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-\text{Cys}-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-\text{Cys}-X_{14}-X_{15}-X_{16}$ (SEQ ID NO:4), and the following amino acid positions are independently selected as follows: X_1 is Ser; X_2 is Arg; X_3 is Asn or Asp; X_7 is Asp; X_8 is Glu or Pro; X_9 is Leu; X_{10} is Thr; X_{14} is Leu; X_{15} is His, Leu, or Pro; X_{16} is Asp or Ser; or combinations of such selections; or

(e) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-\text{Cys}-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-\text{Cys}-X_{16}-X_{17}-X_{18}$ (SEQ ID NO:5), and the following amino acid positions are independently selected as follows: X_1 is Arg; X_2 is Asn, Asp, Gly, or Pro; X_3 is Gly or Met; X_5 is Trp, Tyr, or Val; X_6 is Asp; X_7 is Asp; X_8 is Leu; X_9 is Leu or Thr; X_{10} is Lys or Thr; X_{11} is Arg or Leu; X_{12} is Thr or Trp; X_{13} is Met or Phe; X_{14} is Val; X_{16} is Met; X_{17} is Arg, His, or Tyr; X_{18} is Asn or His; or combinations of such selections; or

(f) said polypeptide includes an amino acid sequence of the following formula:

$X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}$ (SEQ ID NO:6), and the following amino acid positions are independently selected as follows: X_1 is Gly, Tyr, or Val; X_2 is

His or Tyr; X₃ is Asp or Tyr; X₄ is Asp or Gln; X₅ is Leu or Ser; X₆ is Leu or Thr; X₇ is Lys or Thr; X₈ is Leu or Lys; X₉ is Met or Ser; X₁₀ is Thr or Leu; X₁₁ is Pro or Thr; X₁₂ is Arg or Pro; or combinations of such selections; or

(g) said polypeptide includes an amino acid sequence of the following formula:

X₁—X₂—X₃—X₄—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—X₁₃ (SEQ ID NO:7), and the following amino acid positions are independently selected as follows: X₁ is Glu or Lys; X₂ is His or Pro; X₃ is Tyr; X₄ is Asp or Gln; X₅ is Asn or Thr; X₆ is Asp or Pro; X₇ is Ile or Pro; X₈ is Leu or Thr; X₉ is Lys; X₁₀ is Gly or Met; X₁₁ is Ala or Thr; X₁₂ is Arg or His; X₁₃ is His; or combinations of such selections.

13. The BLyS binding polypeptide according to Claim 11, comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 20-162 as depicted in Tables 1-8.

14. The BLyS binding polypeptide according to Claim 11, comprising an amino acid sequence selected from the group consisting of:

AGKEPCYFYWECAVSGPGPEGGGK (SEQ ID NO:163),
AGVPFCDLLTKHCFEAGPGPEGGGK (SEQ ID NO:164),
GSSRLCHMDELTHVCVHFAPPGPEGGGK (SEQ ID NO:165),
DGGGNCYTDSSLTKLHFCMGDEPGPEGGGK (SEQ ID NO:166),
GYDVLTKLYFVPGGPGPEGGGK (SEQ ID NO:167), and
WTDSLTLWFPDGGPGPEGGGK, (SEQ ID NO:168).

15. A recombinant bacteriophage expressing exogenous DNA encoding a BLyS binding polypeptide comprising an amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.

16. The bacteriophage according to Claim 15, wherein Xaa is Pro or Ser.

17. The bacteriophage according to Claim 15, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

Ala-Gly-Lys-Glu-Pro-Cys-Tyr-Phe-Tyr-Trp-Glu-Cys-Ala-Val-Ser-Gly (SEQ ID NO:450);
Ala-Gly-Val-Pro-Phe-Cys-Asp-Leu-Leu-Thr-Lys-His-Cys-Phe-Glu-Ala-Gly (SEQ ID NO:451);
Gly-Ser-Ser-Arg-Leu-Cys-His-Met-Asp-Glu-Leu-Thr-His-Val-Cys-Val-His-Phe-Ala-Pro (SEQ ID NO:452);
Gly-Asp-Gly-Gly-Asn-Cys-Tyr-Thr-Asp-Ser-Leu-Thr-Lys-Leu-His-Phe-Cys-Met-Gly-Asp-Glu (SEQ ID NO:453);
Gly-Tyr-Asp-Val-Leu-Thr-Lys-Leu-Tyr-Phe-Val-Pro-Gly-Gly (SEQ ID NO:454);
Trp-Thr-Asp-Ser-Leu-Thr-Gly-Leu-Trp-Phe-Pro-Asp-Gly-Gly (SEQ ID NO:455);
Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:186);
Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:456);
Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:457);
Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Val (SEQ ID NO:189);
Ala-Asn-Trp-Phe-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:309);
Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Ser-Leu-Pro-Asp (SEQ ID NO:458);
Ala-Asn-Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Phe-Pro-Asp (SEQ ID NO:353);
Ala-Asn-Trp-Tyr-Asp-Ser-Leu-Thr-Lys-Leu-Trp-Leu-Pro-Asp (SEQ ID NO:327).

18. The bacteriophage according to Claim 15, wherein said polypeptides comprises the amino acid sequence: $X_1-X_2-\text{Asp}-X_4-\text{Leu}-\text{Thr}-X_7-\text{Leu}-X_9-X_{10}$ (SEQ ID NO:448), wherein

X_1 is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;
 X_2 is Tyr, Phe, Glu, Cys, Asn;
 X_4 is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;
 X_7 is Lys, Asn, Gln, Gly, or Arg;
 X_9 is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and
 X_{10} is Leu, Phe, Val, Ile, or His.

19. The bacteriophage according to Claim 18, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

20. The bacteriophage according to Claim 18, wherein said polypeptide comprises the amino acid sequence: Ala-X₂-X₃-X₄-Asp-X₆-Leu-Thr-X₉-Leu-X₁₁-X₁₂-X₁₃-X₁₄ (SEQ ID NO:447),

wherein

X₂ is any amino acid except Arg;

X₃ is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X₄ is Tyr, Phe, Glu, Cys, Asn;

X₆ is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X₉ is Lys, Asn, Gln, Gly, or Arg;

X₁₁ is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X₁₂ is Leu, Phe, Val, Ile, or His;

X₁₃ is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X₁₄ is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

21. The bacteriophage according to Claim 18, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 186-435 as depicted in Table 14.

22. A recombinant bacteriophage expressing exogenous DNA encoding a BLyS binding polypeptide comprising an amino acid sequence of the formula:

(A) X₁-X₂-X₃-Cys-X₅-Phe-X₇-Trp-Glu-Cys-X₁₁-X₁₂-X₁₃ (SEQ ID NO:1),

wherein

X₁ is Ala, Asn, Lys, or Ser;

X₂ is Ala, Glu, Met, Ser, or Val;

X₃ is Ala, Asn, Lys, or Pro;

X₅ is Phe, Trp, or Tyr;

X₇ is Pro or Tyr;

X₁₁ is Ala, Gln, His, Phe, or Val;

X₁₂ is Asn, Gln, Gly, His, Ser, or Val; and

X₁₃ is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) $X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-Cys-X_{12}-X_{13}-X_{14}$ (SEQ ID NO:2),

wherein

X_1 is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val, or is absent;

X_2 is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val;

X_3 is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val;

X_5 is Asp, Ile, Leu, or Tyr;

X_6 is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X_7 is His, Leu, Lys, or Phe;

X_8 is Leu, Pro, or Thr;

X_9 is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X_{10} is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X_{12} is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X_{13} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val; and

X_{14} is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is absent; or

(C) $X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-Cys-X_{13}-X_{14}-X_{15}$ (SEQ ID NO:3),

wherein

X_1 is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X_2 is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X_3 is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X_5 is Asn, Asp, Pro, Ser, or Thr;

X_6 is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X_7 is Ala, Ile, Leu, Pro, Thr, or Val;

X_8 is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X_9 is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X₁₀ is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X₁₁ is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X₁₃ is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X₁₄ is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X₁₅ is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—Cys—X₁₄—X₁₅—X₁₆

(SEQ ID NO:4),

wherein

X₁ is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X₂ is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X₃ is Asn, Asp, Leu, Pro, Ser, or Val;

X₅ is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X₆ is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X₇ is Asp, His, Leu, or Ser;

X₈ is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X₉ is Ala, Arg, Asn, or Leu;

X₁₀ is Ile, Leu, Met, Pro, Ser, or Thr;

X₁₁ is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X₁₂ is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X₁₄ is Asp, Gly, Leu, Phe, Tyr, or Val;

X₁₅ is Asn, His, Leu, Pro, or Tyr; and

X₁₆ is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—X₁₃—X₁₄—Cys—X₁₆—X₁₇—X₁₈

(SEQ ID NO:5),

wherein

X₁ is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X₂ is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X₃ is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;

X₅ is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;

X₆ is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;

X₇ is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;

X₈ is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;
X₉ is Asp, Leu, Pro, Thr, or Val;
X₁₀ is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;
X₁₁ is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;
X₁₂ is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;
X₁₃ is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;
X₁₄ is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;
X₁₅ is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;
X₁₆ is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr; and
X₁₈ is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F) X₁—X₂—X₃—X₄—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂ (SEQ ID NO:6),

wherein

X₁ is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;
X₂ is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;
X₃ is Ala, Asp, Lys, Phe, Thr, Trp or Tyr;
X₄ is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;
X₅ is Asp, Leu, Lys, Phe, Pro, Ser, or Val;
X₆ is His, Ile, Leu, Pro, Ser, or Thr;
X₇ is Arg, Gly, His, Leu, Lys, Met, or Thr;
X₈ is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;
X₉ is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;
X₁₀ is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;
X₁₁ is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and
X₁₂ is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G) X₁—X₂—X₃—X₄—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—X₁₃ (SEQ ID NO:7),

wherein

X₁ is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;
X₂ is Arg, Gln, His, Ile, Leu, or Pro;
X₃ is Asp, Gly, Ile, Lys, Thr, Tyr or Val;
X₄ is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;
X₅ is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;

X₆ is Asp, Glu, His, Leu, Lys, Pro, or Val;
X₇ is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;
X₈ is Gln, Gly, His, Leu, Met, Ser, or Thr;
X₉ is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;
X₁₀ is Ala, Gly, Ile, Leu, Lys, Met, or Phe;
X₁₁ is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;
X₁₂ is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and
X₁₃ is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

23. The recombinant bacteriophage according to Claim 22, wherein

(a) said polypeptide comprises an amino acid sequence of the following formula:

X₁—X₂—X₃—Cys—X₅—Phe—X₇—Trp—Glu—Cys—X₁₁—X₁₂—X₁₃ (SEQ ID NO:1), and the following amino acid positions are independently selected as follows: X₃ is Lys; X₅ is Tyr; X₇ is Pro; X₁₁ is Ala, Gln, His, Phe, or Val; X₁₂ is Asn, Gln, Gly, His, Ser, or Val; X₁₃ is Ala, Asn, Gly, Ile, Pro, or Ser; or combinations of such selections; or

(b) said polypeptide comprises an amino acid sequence of the following formula:

X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—Cys—X₁₂—X₁₃—X₁₄ (SEQ ID NO:2), and the following amino acid positions are independently selected as follows: X₃ is Asp; X₅ is Asp or Leu; X₆ is Glu or Leu; X₇ is His or Leu; X₈ is Thr or Pro; X₉ is Lys; or combinations of such selections; or

(c) said polypeptide comprises an amino acid sequence of the following formula:

X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—Cys—X₁₃—X₁₄—X₁₅ (SEQ ID NO:3), and the following amino acid positions are independently selected as follows: X₃ is Ala; X₅ is Asp; X₆ is Ile; X₇ is Val or Leu; X₈ is Thr; X₉ is Leu; X₁₁ is Ser; X₁₃ is Val; X₁₅ is Glu or Pro; or combinations of such selections; or

(d) said polypeptide comprises an amino acid sequence of the following formula:

X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—Cys—X₁₄—X₁₅—X₁₆ (SEQ ID NO:4), and the following amino acid positions are independently selected as follows: X₁ is Ser; X₂ is Arg; X₃ is Asn or Asp; X₇ is Asp; X₈ is Glu or Pro; X₉ is Leu; X₁₀ is Thr; X₁₄ is Leu; X₁₅ is His, Leu, or Pro; X₁₆ is Asp or Ser; or combinations of such selections; or

(e) said polypeptide comprises an amino acid sequence of the following formula:

$X_1-X_2-X_3-Cys-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-Cys-X_{16}-X_{17}-X_{18}$ (SEQ ID NO:5), and the following amino acid positions are independently selected as follows: X_1 is Arg; X_2 is Asn, Asp, Gly, or Pro; X_3 is Gly or Met; X_5 is Trp, Tyr, or Val; X_6 is Asp; X_7 is Asp; X_8 is Leu; X_9 is Leu or Thr; X_{10} is Lys or Thr; X_{11} is Arg or Leu; X_{12} is Thr or Trp; X_{13} is Met or Phe; X_{14} is Val; X_{16} is Met; X_{17} is Arg, His, or Tyr; X_{18} is Asn or His; or combinations of such selections; or

(f) said polypeptide comprises an amino acid sequence of the following formula:

$X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}$ (SEQ ID NO:6), and the following amino acid positions are independently selected as follows: X_1 is Gly, Tyr, or Val; X_2 is His or Tyr; X_3 is Asp or Tyr; X_4 is Asp or Gln; X_5 is Leu or Ser; X_6 is Leu or Thr; X_7 is Lys or Thr; X_8 is Leu or Lys; X_9 is Met or Ser; X_{10} is Thr or Leu; X_{11} is Pro or Thr; X_{12} is Arg or Pro; or combinations of such selections; or

(g) said polypeptide comprises an amino acid sequence of the following formula:

$X_1-X_2-X_3-X_4-X_5-X_6-X_7-X_8-X_9-X_{10}-X_{11}-X_{12}-X_{13}$ (SEQ ID NO:7), and the following amino acid positions are independently selected as follows: X_1 is Glu or Lys; X_2 is His or Pro; X_3 is Tyr; X_4 is Asp or Gln; X_5 is Asn or Thr; X_6 is Asp or Pro; X_7 is Ile or Pro; X_8 is Leu or Thr; X_9 is Lys; X_{10} is Gly or Met; X_{11} is Ala or Thr; X_{12} is Arg or His; X_{13} is His; or combinations of such selections.

24. A method for detecting BLyS or a BLyS-like polypeptide in a solution suspected of containing it comprising:

- (a) contacting said solution with a polypeptide according to any of Claims 1, 9 or 11, and
- (b) determining whether binding has occurred between said polypeptide and BLyS or a BLyS-like polypeptide.

25. A method for purifying BLyS or a BLyS-like polypeptide comprising:

- (a) immobilizing a binding polypeptide according to any of Claims 1, 9 or 11 on a solid support;
- (b) contacting a solution containing BLyS or a BLyS-like polypeptide with said support; and, thereafter,
- (c) separating the solution from said support.

26. BLyS separation media comprising:

- (a) a chromatographic matrix material, and, immobilized thereon,
- (b) a BLyS binding molecule comprising a BLyS binding polypeptide as defined in any of Claims 1, 9 or 11.

27. The BLyS separation media according to Claim 26, comprising:

- (a) a chromatographic matrix material, and, immobilized thereon,
- (b) a BLyS binding molecule comprising a BLyS binding polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:20-162 and 186-435, as depicted in Tables 1-8 and 14.

28. A method for separating BLyS or a BLyS-like polypeptide from a solution containing it comprising:

- (a) contacting said solution with separation media as defined in Claim 26,
- (b) removing unbound material, and
- (c) eluting bound BLyS or BLyS-like polypeptide from said separation media.

29. A polynucleotide encoding a BLyS binding polypeptide comprising the amino acid sequence: Asp-Xaa-Leu-Thr (SEQ ID NO:446), wherein Xaa is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala.

30. The polynucleotide according to Claim 29, wherein Xaa is Pro or Ser.

31. The polynucleotide according to Claim 29, wherein said polypeptides comprises the amino acid sequence: X₁-X₂-Asp-X₄-Leu-Thr-X₇-Leu-X₉-X₁₀ (SEQ ID NO:448), wherein

X₁ is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X₂ is Tyr, Phe, Glu, Cys, Asn;

X₄ is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X₇ is Lys, Asn, Gln, Gly, or Arg;

X₉ is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys; and
X₁₀ is Leu, Phe, Val, Ile, or His.

32. The polynucleotide according to Claim 31, wherein said polypeptide comprises the amino acid sequence: Trp-Tyr-Asp-Pro-Leu-Thr-Lys-Leu-Trp-Leu (SEQ ID NO:436).

33. The polynucleotide according to Claim 31, wherein said polypeptide comprises the amino acid sequence: Ala-X₂-X₃-X₄-Asp-X₆-Leu-Thr-X₉-Leu-X₁₁-X₁₂-X₁₃-X₁₄ (SEQ ID NO:447),

wherein

X₂ is any amino acid except Arg;

X₃ is Trp, Glu, Lys, Cys, Leu, Ala, Arg, Gly, or Ser;

X₄ is Tyr, Phe, Glu, Cys, Asn;

X₆ is Pro, Ser, Thr, Phe, Leu, Tyr, Cys, or Ala;

X₉ is Lys, Asn, Gln, Gly, or Arg;

X₁₁ is Trp, Ser, Thr, Arg, Cys, Tyr, or Lys;

X₁₂ is Leu, Phe, Val, Ile, or His;

X₁₃ is Pro, Leu, His, Ser, Arg, Asn, Gln, Thr, Val, Ala, Cys, Ile, Phe, or Tyr; and

X₁₄ is Asp, Glu, Asn, Val, His, Gln, Arg, Gly, Ser, Tyr, Ala, Cys, Lys, Ile, Thr or Leu.

34. The polynucleotide according to Claim 31, encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 186-435 as depicted in Table 14.

35. A polynucleotide encoding a BLyS binding polypeptide of the formula:

(A) X₁-X₂-X₃-Cys-X₅-Phe-X₇-Trp-Glu-Cys-X₁₁-X₁₂-X₁₃ (SEQ ID NO:1),

wherein

X₁ is Ala, Asn, Lys, or Ser;

X₂ is Ala, Glu, Met, Ser, or Val;

X₃ is Ala, Asn, Lys, or Pro;

X₅ is Phe, Trp, or Tyr;

X₇ is Pro or Tyr;

X₁₁ is Ala, Gln, His, Phe, or Val;

X₁₂ is Asn, Gln, Gly, His, Ser, or Val; and

X₁₃ is Ala, Asn, Gly, Ile, Pro, or Ser; or

(B) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—Cys—X₁₂—X₁₃—X₁₄ (SEQ ID NO:2),
wherein

X₁ is Ala, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, Val,
or is absent;

X₂ is Ala, Asn, Asp, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or
Val;

X₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr,
or Val;

X₅ is Asp, Ile, Leu, or Tyr;

X₆ is Arg, Asp, Glu, His, Ile, Leu, Lys, Phe, Pro, Tyr, or Val;

X₇ is His, Leu, Lys, or Phe;

X₈ is Leu, Pro, or Thr;

X₉ is Arg, Asn, Gly, His, Ile, Lys, Met, or Trp;

X₁₀ is Ala, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Ser, Trp, Tyr, or Val;

X₁₂ is Asp, Gln, Glu, Gly, Ile, Leu, Lys, Phe, Ser, Trp, Tyr, or Val;

X₁₃ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp,
Tyr, or Val; and

X₁₄ is Ala, Arg, Asn, Asp, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Trp, Tyr, Val, or is
absent; or

(C) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—Cys—X₁₃—X₁₄—X₁₅ (SEQ ID NO:3),
wherein

X₁ is Ala, Arg, Asn, Asp, Leu, Lys, Phe, Pro, Ser, or Thr;

X₂ is Asn, Asp, Gln, His, Ile, Lys, Pro, Thr, or Trp;

X₃ is Ala, Arg, Asn, Gln, Glu, His, Phe, Pro, or Thr;

X₅ is Asn, Asp, Pro, Ser, or Thr;

X₆ is Arg, Asp, Ile, Leu, Met, Pro, or Val;

X₇ is Ala, Ile, Leu, Pro, Thr, or Val;

X₈ is Asn, His, Ile, Leu, Lys, Phe, or Thr;

X₉ is Asn, Glu, Gly, His, Leu, Lys, Met, Pro, or Thr;

X₁₀ is Arg, Asn, Asp, Gln, Glu, Gly, Ile, Lys, Met, Pro, Ser, or Trp;

X₁₁ is Arg, Glu, Gly, Lys, Phe, Ser, Trp, or Tyr;

X₁₃ is Gln, Glu, Ile, Leu, Phe, Pro, Ser, Tyr, or Val;

X₁₄ is Asn, Gly, Ile, Phe, Pro, Thr, Trp, or Tyr; and

X₁₅ is Asn, Asp, Glu, Leu, Lys, Met, Pro, or Thr; or

(D) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—Cys—X₁₄—X₁₅—X₁₆ (SEQ ID NO:4),

wherein

X₁ is Asn, Asp, His, Leu, Phe, Pro, Ser, Tyr, or is absent;

X₂ is Arg, Asn, Asp, His, Phe, Ser, or Trp;

X₃ is Asn, Asp, Leu, Pro, Ser, or Val;

X₅ is Asp, Gln, His, Ile, Leu, Lys, Met, Phe, or Thr;

X₆ is His, Ile, Leu, Met, Phe, Pro, Trp, or Tyr;

X₇ is Asp, His, Leu, or Ser;

X₈ is Ala, Arg, Asp, Glu, Leu, Phe, Pro, or Thr;

X₉ is Ala, Arg, Asn, or Leu;

X₁₀ is Ile, Leu, Met, Pro, Ser, or Thr;

X₁₁ is Ala, Arg, Asn, Gly, His, Lys, Ser, or Tyr;

X₁₂ is Ala, Arg, Asn, Gln, Leu, Met, Ser, Trp, Tyr, or Val;

X₁₄ is Asp, Gly, Leu, Phe, Tyr, or Val;

X₁₅ is Asn, His, Leu, Pro, or Tyr; and

X₁₆ is Asn, Asp, His, Phe, Ser, or Tyr; or

(E) X₁—X₂—X₃—Cys—X₅—X₆—X₇—X₈—X₉—X₁₀—X₁₁—X₁₂—X₁₃—X₁₄—Cys—X₁₆—X₁₇—X₁₈ (SEQ ID NO:5),

wherein

X₁ is Arg, Asp, Gly, His, Leu, Phe, Pro, Ser, Trp, Tyr, or is absent;

X₂ is Ala, Arg, Asn, Asp, Gly, Pro, Ser, or is absent;

X₃ is Arg, Asn, Gln, Glu, Gly, Lys, Met, Pro, Trp or Val;

X₅ is Arg, Asn, Gln, Glu, His, Leu, Phe, Pro, Trp, Tyr, or Val;
X₆ is Arg, Asp, Gln, Gly, Ile, Lys, Phe, Thr, Trp or Tyr;
X₇ is Ala, Arg, Asp, Glu, Gly, Leu, Ser, or Tyr;
X₈ is Asp, Gln, Glu, Leu, Met, Phe, Pro, Ser, or Tyr;
X₉ is Asp, Leu, Pro, Thr, or Val;
X₁₀ is Arg, Gln, His, Ile, Leu, Lys, Met, Phe, Thr, Trp or Tyr;
X₁₁ is Ala, Arg, Asn, Gln, Glu, His, Leu, Lys, Met, or Thr;
X₁₂ is Ala, Asn, Gln, Gly, Leu, Lys, Phe, Pro, Thr, Trp, or Tyr;
X₁₃ is Ala, Arg, Gln, His, Lys, Met, Phe, Pro, Thr, Trp, or Tyr;
X₁₄ is Arg, Gln, Glu, Gly, His, Leu, Met, Phe, Pro, Ser, Thr, Tyr, or Val;
X₁₅ is Arg, Asp, Gly, His, Lys, Met, Phe, Pro, Ser, or Trp;
X₁₆ is Arg, Asn, Asp, Gly, His, Phe, Pro, Ser, Trp or Tyr; and
X₁₇ is Ala, Arg, Asn, Asp, His, Leu, Phe, or Trp; or

(F) X₁–X₂–X₃–X₄–X₅–X₆–X₇–X₈–X₉–X₁₀–X₁₁–X₁₂ (SEQ ID NO:6),
wherein

X₁ is Ala, Arg, Gly, His, Leu, Lys, Met, Phe, Trp, Tyr, or Val;
X₂ is Ala, Arg, Gln, His, Ile, Leu, Phe, Thr, Trp, or Tyr;
X₃ is Ala, Asp, Lys, Phe, Thr, Trp or Tyr;
X₄ is Arg, Asp, Gln, Lys, Met, Phe, Pro, Ser, Tyr, or Val;
X₅ is Asp, Leu, Lys, Phe, Pro, Ser, or Val;
X₆ is His, Ile, Leu, Pro, Ser, or Thr;
X₇ is Arg, Gly, His, Leu, Lys, Met, or Thr;
X₈ is Ala, Arg, Asn, Ile, Leu, Lys, Met, or Thr;
X₉ is Ala, Asn, Arg, Asp, Glu, Gly, His, Leu, Met, Ser, Trp, Tyr, or Val;
X₁₀ is Ile, Leu, Phe, Ser, Thr, Trp, Tyr, or Val;
X₁₁ is Ala, Arg, Gly, His, Ile, Leu, Lys, Pro, Ser, Thr, Trp, Tyr, or Val; and
X₁₂ is Arg, Asp, His, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val; or

(G) X₁–X₂–X₃–X₄–X₅–X₆–X₇–X₈–X₉–X₁₀–X₁₁–X₁₂–X₁₃ (SEQ ID NO:7),
wherein

X₁ is Asp, Gln, Glu, Gly, His, Lys, Met, or Trp;
X₂ is Arg, Gln, His, Ile, Leu, or Pro;

X₃ is Asp, Gly, Ile, Lys, Thr, Tyr or Val;
X₄ is Asn, Asp, Gln, Glu, Met, Pro, Ser, or Tyr;
X₅ is Asn, Asp, His, Ile, Leu, Met, Pro, Thr or Val;
X₆ is Asp, Glu, His, Leu, Lys, Pro, or Val;
X₇ is Arg, Asn, Gln, His, Ile, Leu, Met, Pro, or Thr;
X₈ is Gln, Gly, His, Leu, Met, Ser, or Thr;
X₉ is Asn, Gln, Gly, His, Leu, Lys, Ser, or Thr;
X₁₀ is Ala, Gly, Ile, Leu, Lys, Met, or Phe;
X₁₁ is Ala, Glu, His, Ile, Leu, Met, Ser, Thr, Trp, Tyr, or Val;
X₁₂ is Arg, Gln, Glu, Gly, His, Ile, Lys, Tyr, or Val; and
X₁₃ is Arg, Asn, Glu, His, Ile, Ser, Thr, Trp, or Val.

36. A method for identifying a binding molecule for a BLyS target comprising the steps of utilizing a BLyS binding polypeptide according to any of Claims 1, 9 or 11 to form a complex with BLyS or a BLyS-like polypeptide, contacting said complex with one or more potential BLyS target binding molecules, and determining whether said one or more potential BLyS target binding molecules competes with said BLyS binding polypeptide to form a complex with said BLyS or BLyS-like polypeptide.

37. A BLyS affinity maturation library, comprising a population of at least 10³ polypeptides, wherein the polypeptides of said population comprise the amino acid sequence:

Ala-X₂-X₃-X₄-Asp-X₆-Leu-Thr-X₉-Leu-X₁₁-X₁₂-X₁₃-X₁₄ (SEQ ID NO:449),
wherein

X₂ is any amino acid;
X₃ is any amino acid;
X₄ is any amino acid;
X₆ is any amino acid;
X₉ is any amino acid;
X₁₁ is any amino acid;

X₁₂ is any amino acid;
X₁₃ is any amino acid; and
X₁₄ is any amino acid.

38. A DNA template encoding a multiplicity of BLyS binding polypeptides, comprising the sequence:

GCT NNN NNN NNN GAT NNN CTT ACT NNN CTC NNN NNN NNN NNN (SEQ ID NO:185).